

Mor0003.ST25.txt  
SEQUENCE LISTING



<110> Nicolaides, Nicholas C.  
Grasso, Luigi  
Sass, Philip M.

<120> Methods For Generating Genetically Altered Antibody-Producing  
Cell Lines With Improved Antibody Characteristics

<130> MOR-0003

<140> US 09/707,468

<141> 2000-11-07

<160> 23

<170> PatentIn version 3.2

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<213> Artificial Sequence

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<223> Oligonucleotide primer

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 35 40 45

Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp  
 50 55 60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
 65 70 75 80

Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
 85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser  
 100 105 110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser  
 115 120 125

Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr  
 130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln  
 145 150 155 160

His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn  
 165 170 175

Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys  
 180 185 190

Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln  
 195 200 205

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Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys  
 210 215 220  
 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile  
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 Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly  
 245 250 255  
 Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser  
 260 265 270  
 Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser  
 275 280 285  
 Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser  
 290 295 300  
 Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
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 Val Val Leu Asn Val Ser Val Asp Ser Glu Cys Val Asp Ile Asp Val  
 325 330 335  
 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
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 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn  
 355 360 365  
 Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
 370 375 380  
 Val Lys Leu His Thr Ala Glu Leu Glu Lys Pro Val Pro Gly Lys Gln  
 385 390 395 400  
 Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala  
 405 410 415  
 Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu  
 420 425 430  
 Ile Lys Ser Arg Gly Pro Glu Thr Ala Glu Leu Thr Arg Ser Phe Pro  
 435 440 445  
 Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Asp  
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 Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp  
 465 470 475 480

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Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly  
485 490 495

Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Glu Phe Ser Thr Pro Glu  
500 505 510

Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp  
515 520 525

Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Arg Pro  
530 535 540

Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys  
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Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe  
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Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro  
580 585 590

Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met  
595 600 605

Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu  
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Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu  
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Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala  
645 650 655

Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu  
660 665 670

Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu  
675 680 685

Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr  
690 695 700

Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu  
705 710 715 720

Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu  
725 730 735

Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile  
740 745 750

Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro  
755 760 765

Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile  
 770 775 780

Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val  
 785 790 795 800

Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly  
 805 810 815

Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly  
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Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg  
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35      40      45

Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp
50      55      60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
65      70      75      80

Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
85      90      95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
100     105     110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser
115     120     125

Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile
130     135     140

Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln
145     150     155     160

Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn
165     170     175

Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys
180     185     190

Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
195     200     205

Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys
210     215     220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
225     230     235     240

Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly
245     250     255

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Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
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Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val
325                               330                335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu
340                               345                350

Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn
355                               360                365

Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu
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Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser
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Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu Arg His Thr Thr Glu Asn
420                               425                430

Lys Pro His Ser Pro Lys Thr Pro Glu Pro Arg Arg Ser Pro Leu Gly
435                               440                445

Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp
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Lys Gly Val Leu Arg Pro Gln Lys Glu Ala Val Ser Ser Ser His Gly
465                               470                475                480

Pro Ser Asp Pro Thr Asp Arg Ala Glu Val Glu Lys Asp Ser Gly His
485                               490                495

Gly Ser Thr Ser Val Asp Ser Glu Gly Phe Ser Ile Pro Asp Thr Gly
500                               505                510

Ser His Cys Ser Ser Glu Tyr Ala Ala Ser Ser Pro Gly Asp Arg Gly
515                               520                525

Ser Gln Glu His Val Asp Ser Gln Glu Lys Ala Pro Glu Thr Asp Asp
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Ser Phe Ser Asp Val Asp Cys His Ser Asn Gln Glu Asp Thr Gly Cys
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Lys Phe Arg Val Leu Pro Gln Pro Thr Asn Leu Ala Thr Pro Asn Thr  
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 Lys Arg Phe Lys Lys Glu Glu Ile Leu Ser Ser Ser Asp Ile Cys Gln  
 580 585 590  
 Lys Leu Val Asn Thr Gln Asp Met Ser Ala Ser Gln Val Asp Val Ala  
 595 600 605  
 Val Lys Ile Asn Lys Lys Val Val Pro Leu Asp Phe Ser Met Ser Ser  
 610 615 620  
 Leu Ala Lys Arg Ile Lys Gln Leu His His Glu Ala Gln Gln Ser Glu  
 625 630 635 640  
 Gly Glu Gln Asn Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu  
 645 650 655  
 Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met  
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 Phe Ala Glu Met Glu Ile Ile Gly Gln Phe Asn Leu Gly Phe Ile Ile  
 675 680 685  
 Thr Lys Leu Asn Glu Asp Ile Phe Ile Val Asp Gln His Ala Thr Asp  
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 Glu Lys Tyr Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Gly  
 705 710 715 720  
 Gln Arg Leu Ile Ala Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu  
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 Ala Val Leu Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp  
 740 745 750  
 Phe Val Ile Asp Glu Asn Ala Pro Val Thr Glu Arg Ala Lys Leu Ile  
 755 760 765  
 Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp  
 770 775 780  
 Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro  
 785 790 795 800  
 Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val  
 805 810 815  
 Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr  
 820 825 830

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His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro  
835 840 845

Thr Met Arg His Ile Ala Asn Leu Gly Val Ile Ser Gln Asn  
850 855 860

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## Mor0003.ST25.txt

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```

Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser
20          25          30

```

```

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly
35          40          45

```

```

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val
50          55          60

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```

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser
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His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
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Mor0003.ST25.txt

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 Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser  
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 Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu  
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 Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His  
 180 185 190  
 Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met  
 195 200 205  
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 Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu  
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 290 295 300  
 Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln  
 305 310 315 320  
 Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys  
 325 330 335  
 Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp  
 340 345 350  
 Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val  
 355 360 365  
 Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp  
 370 375 380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly  
 385 390 395 400  
 Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe  
 405 410 415  
 Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr  
 420 425 430  
 Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn  
 435 440 445  
 Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His  
 450 455 460  
 Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu  
 465 470 475 480  
 Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp  
 485 490 495  
 Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile  
 500 505 510  
 Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val  
 515 520 525  
 Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp  
 530 535 540  
 Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val  
 545 550 555 560  
 Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser  
 565 570 575  
 Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu  
 580 585 590  
 Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu  
 595 600 605  
 Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala  
 610 615 620  
 Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu  
 625 630 635 640  
 Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro  
 645 650 655

## Mor0003.ST25.txt

Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu  
 660 665 670  
 Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys  
 675 680 685  
 Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys  
 690 695 700  
 Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu  
 705 710 715 720  
 Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp  
 725 730 735  
 Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val  
 740 745 750  
 Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro  
 755 760 765  
 Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn  
 770 775 780  
 Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln  
 785 790 795 800  
 Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn  
 805 810 815  
 Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr  
 820 825 830  
 Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala  
 835 840 845  
 Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu  
 850 855 860  
 Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu  
 865 870 875 880  
 Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Tyr Glu Asp  
 885 890 895  
 Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile  
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 915 920 925  
 Pro Glu Thr Thr  
 930

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 <212> DNA  
 <213> Homo sapiens

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 gttctcagat catcacttcg gtggtcagtg ttgtaaaaga gcttattgaa aactccttgg 180  
 atgctggtgc cacaagcgta gatgttaaac tggagaacta tggatttgat aaaattgagg 240  
 tgcgagataa cggggagggt atcaaggctg ttgatgcacc tgtaatggca atgaagtact 300  
 acacctcaaa aataaatagt catgaagatc ttgaaaattt gacaacttac ggttttcgtg 360  
 gagaagcctt ggggtcaatt tgttgatatag ctgaggtttt aattacaaca agaacggctg 420  
 ctgataattt tagcaccag tatgttttag atggcagtg ccacatactt tctcagaaac 480  
 cttcacatct tgggtcaagg acaactgtaa ctgctttaag attatttaag aatctacctg 540  
 taagaaagca gttttactca actgcaaaaa aatgtaaaga tgaaataaaa aagatccaag 600  
 atctcctcat gagctttggt atccttaaac ctgacttaag gattgtcttt gtacataaca 660  
 aggcagttat ttggcagaaa agcagagtat cagatcaca gatggctctc atgtcagttc 720  
 tggggactgc tggtatgaac aatatggaat cctttcagta cactctgaa gaatctcaga 780  
 tttatctcag tggatttctt ccaaagtgtg atgcagacca ctctttcact agtctttcaa 840  
 caccagaaag aagtttcatc ttcataaaca gtcgaccagt acatcaaaaa gatattctaa 900  
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 cgacttggtt tggaccatta ctagtataa attcttatga aaataataaa acagatgttt 1140  
 ccgcagctga catcgttctt agtaaaacag cagaaacaga tgtgcttttt aataaagtgg 1200  
 aatcatctgg aaagaattat tcaaatgtt atacttcagt cattccattc caaaatgata 1260  
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 gtgactttgg ttatggtcat tgtagtagtg aaatttctaa cattgataaa aacactaaga 1380  
 atgcatttca ggacatttca atgagtaatg tatcatggga gaactctcag acggaatata 1440  
 gtaaaacttg ttttataagt tccgttaagc acaccagtc agaaaatggc aataaagacc 1500  
 atatagatga gagtggggaa aatgaggaag aagcaggtct tgaaaactct tcggaaattt 1560  
 ctgcagatga gtggagcagg ggaaatatac taaaaaatc agtgggagag aatattgaac 1620  
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 caatccctga acaaatgaat cttaatgaag attcatgtaa caaaaaatca aatgtaatag 1740  
 ataataaatc tggaaaagtt acagcttatg atttacttag caatcgagta atcaagaaac 1800  
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## Mor0003.ST25.txt

ctaagactag tttagaggat gcaacactac aaattgaaga actgtggaag acattgagtg 1920  
 aagaggaaaa actgaaatat gaagagaagg ctactaaaga cttggaacga tacaatagtc 1980  
 aaatgaagag agccattgaa caggagtcac aaatgtcact aaaagatggc agaaaaaaga 2040  
 taaaaccac cagcgcatgg aatttgccc agaagcaca gttaaaaacc tcattatcta 2100  
 atcaaccaa acttgatgaa ctcttcagt cccaaattga aaaaagaagg agtcaaaata 2160  
 ttaaatgggt acagatcccc ttttctatga aaaacttaaa aataaatttt aagaaacaaa 2220  
 acaaagttga cttagaagag aaggatgaac cttgcttgat ccacaatctc aggtttcctg 2280  
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 aagccctgct atttaaaaga cttcttgaga atcataaact tcctgcagag cactggaaa 2400  
 agccaattat gttaacagag agtcttttta atggatctca ttatttagac gttttatata 2460  
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 taaatatgtt taagaagatt agttaccatt gaaattgggt ctgtcataaa acagcatgag 2940  
 tctggtttta aattatcttt gtattatgtg tcacatgggt attttttaaa tgaggattca 3000  
 ctgacttggt tttatattga aaaaagttcc acgtattgta gaaaacgtaa ataaactaat 3060  
 aac 3063

<210> 11  
 <211> 934  
 <212> PRT  
 <213> Homo sapiens

<400> 11

Met Ala Val Gln Pro Lys Glu Thr Leu Gln Leu Glu Ser Ala Ala Glu  
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Val Gly Phe Val Arg Phe Phe Gln Gly Met Pro Glu Lys Pro Thr Thr  
20 25 30

Thr Val Arg Leu Phe Asp Arg Gly Asp Phe Tyr Thr Ala His Gly Glu  
35 40 45

Asp Ala Leu Leu Ala Ala Arg Glu Val Phe Lys Thr Gln Gly Val Ile  
50 55 60

Lys Tyr Met Gly Pro Ala Gly Ala Lys Asn Leu Gln Ser Val Val Leu  
65 70 75 80

## Mor0003.ST25.txt

Ser Lys Met Asn Phe Glu Ser Phe Val Lys Asp Leu Leu Leu Val Arg  
 85 90 95  
 Gln Tyr Arg Val Glu Val Tyr Lys Asn Arg Ala Gly Asn Lys Ala Ser  
 100 105 110  
 Lys Glu Asn Asp Trp Tyr Leu Ala Tyr Lys Ala Ser Pro Gly Asn Leu  
 115 120 125  
 Ser Gln Phe Glu Asp Ile Leu Phe Gly Asn Asn Asp Met Ser Ala Ser  
 130 135 140  
 Ile Gly Val Val Gly Val Lys Met Ser Ala Val Asp Gly Gln Arg Gln  
 145 150 155 160  
 Val Gly Val Gly Tyr Val Asp Ser Ile Gln Arg Lys Leu Gly Leu Cys  
 165 170 175  
 Glu Phe Pro Asp Asn Asp Gln Phe Ser Asn Leu Glu Ala Leu Leu Ile  
 180 185 190  
 Gln Ile Gly Pro Lys Glu Cys Val Leu Pro Gly Gly Glu Thr Ala Gly  
 195 200 205  
 Asp Met Gly Lys Leu Arg Gln Ile Ile Gln Arg Gly Gly Ile Leu Ile  
 210 215 220  
 Thr Glu Arg Lys Lys Ala Asp Phe Ser Thr Lys Asp Ile Tyr Gln Asp  
 225 230 235 240  
 Leu Asn Arg Leu Leu Lys Gly Lys Lys Gly Glu Gln Met Asn Ser Ala  
 245 250 255  
 Val Leu Pro Glu Met Glu Asn Gln Val Ala Val Ser Ser Leu Ser Ala  
 260 265 270  
 Val Ile Lys Phe Leu Glu Leu Leu Ser Asp Asp Ser Asn Phe Gly Gln  
 275 280 285  
 Phe Glu Leu Thr Thr Phe Asp Phe Ser Gln Tyr Met Lys Leu Asp Ile  
 290 295 300  
 Ala Ala Val Arg Ala Leu Asn Leu Phe Gln Gly Ser Val Glu Asp Thr  
 305 310 315 320  
 Thr Gly Ser Gln Ser Leu Ala Ala Leu Leu Asn Lys Cys Lys Thr Pro  
 325 330 335  
 Gln Gly Gln Arg Leu Val Asn Gln Trp Ile Lys Gln Pro Leu Met Asp  
 340 345 350  
 Lys Asn Arg Ile Glu Glu Arg Leu Asn Leu Val Glu Ala Phe Val Glu  
 355 360 365

Mor0003.ST25.txt

Asp Ala Glu Leu Arg Gln Thr Leu Gln Glu Asp Leu Leu Arg Arg Phe  
 370 375 380  
 Pro Asp Leu Asn Arg Leu Ala Lys Lys Phe Gln Arg Gln Ala Ala Asn  
 385 390 395 400  
 Leu Gln Asp Cys Tyr Arg Leu Tyr Gln Gly Ile Asn Gln Leu Pro Asn  
 405 410 415  
 Val Ile Gln Ala Leu Glu Lys His Glu Gly Lys His Gln Lys Leu Leu  
 420 425 430  
 Leu Ala Val Phe Val Thr Pro Leu Thr Asp Leu Arg Ser Asp Phe Ser  
 435 440 445  
 Lys Phe Gln Glu Met Ile Glu Thr Thr Leu Asp Met Asp Gln Val Glu  
 450 455 460  
 Asn His Glu Phe Leu Val Lys Pro Ser Phe Asp Pro Asn Leu Ser Glu  
 465 470 475 480  
 Leu Arg Glu Ile Met Asn Asp Leu Glu Lys Lys Met Gln Ser Thr Leu  
 485 490 495  
 Ile Ser Ala Ala Arg Asp Leu Gly Leu Asp Pro Gly Lys Gln Ile Lys  
 500 505 510  
 Leu Asp Ser Ser Ala Gln Phe Gly Tyr Tyr Phe Arg Val Thr Cys Lys  
 515 520 525  
 Glu Glu Lys Val Leu Arg Asn Asn Lys Asn Phe Ser Thr Val Asp Ile  
 530 535 540  
 Gln Lys Asn Gly Val Lys Phe Thr Asn Ser Lys Leu Thr Ser Leu Asn  
 545 550 555 560  
 Glu Glu Tyr Thr Lys Asn Lys Thr Glu Tyr Glu Glu Ala Gln Asp Ala  
 565 570 575  
 Ile Val Lys Glu Ile Val Asn Ile Ser Ser Gly Tyr Val Glu Pro Met  
 580 585 590  
 Gln Thr Leu Asn Asp Val Leu Ala Gln Leu Asp Ala Val Val Ser Phe  
 595 600 605  
 Ala His Val Ser Asn Gly Ala Pro Val Pro Tyr Val Arg Pro Ala Ile  
 610 615 620  
 Leu Glu Lys Gly Gln Gly Arg Ile Ile Leu Lys Ala Ser Arg His Ala  
 625 630 635 640

Mor0003.ST25.txt

Cys	Val	Glu	Val	Gln	Asp	Glu	Ile	Ala	Phe	Ile	Pro	Asn	Asp	Val	Tyr
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Phe	Glu	Lys	Asp	Lys	Gln	Met	Phe	His	Ile	Ile	Thr	Gly	Pro	Asn	Met
			660					665					670		
Gly	Gly	Lys	Ser	Thr	Tyr	Ile	Arg	Gln	Thr	Gly	Val	Ile	Val	Leu	Met
		675					680					685			
Ala	Gln	Ile	Gly	Cys	Phe	Val	Pro	Cys	Glu	Ser	Ala	Glu	Val	Ser	Ile
	690					695					700				
Val	Asp	Cys	Ile	Leu	Ala	Arg	Val	Gly	Ala	Gly	Asp	Ser	Gln	Leu	Lys
705					710					715					720
Gly	Val	Ser	Thr	Phe	Met	Ala	Glu	Met	Leu	Glu	Thr	Ala	Ser	Ile	Leu
				725					730					735	
Arg	Ser	Ala	Thr	Lys	Asp	Ser	Leu	Ile	Ile	Ile	Asp	Glu	Leu	Gly	Arg
			740					745					750		
Gly	Thr	Ser	Thr	Tyr	Asp	Gly	Phe	Gly	Leu	Ala	Trp	Ala	Ile	Ser	Glu
		755					760					765			
Tyr	Ile	Ala	Thr	Lys	Ile	Gly	Ala	Phe	Cys	Met	Phe	Ala	Thr	His	Phe
	770					775					780				
His	Glu	Leu	Thr	Ala	Leu	Ala	Asn	Gln	Ile	Pro	Thr	Val	Asn	Asn	Leu
785					790					795					800
His	Val	Thr	Ala	Leu	Thr	Thr	Glu	Glu	Thr	Leu	Thr	Met	Leu	Tyr	Gln
				805					810					815	
Val	Lys	Lys	Gly	Val	Cys	Asp	Gln	Ser	Phe	Gly	Ile	His	Val	Ala	Glu
			820					825					830		
Leu	Ala	Asn	Phe	Pro	Lys	His	Val	Ile	Glu	Cys	Ala	Lys	Gln	Lys	Ala
		835					840					845			
Leu	Glu	Leu	Glu	Glu	Phe	Gln	Tyr	Ile	Gly	Glu	Ser	Gln	Gly	Tyr	Asp
	850					855					860				
Ile	Met	Glu	Pro	Ala	Ala	Lys	Lys	Cys	Tyr	Leu	Glu	Arg	Glu	Gln	Gly
865					870					875					880
Glu	Lys	Ile	Ile	Gln	Glu	Phe	Leu	Ser	Lys	Val	Lys	Gln	Met	Pro	Phe
				885					890					895	
Thr	Glu	Met	Ser	Glu	Glu	Asn	Ile	Thr	Ile	Lys	Leu	Lys	Gln	Leu	Lys
			900					905						910	
Ala	Glu	Val	Ile	Ala	Lys	Asn	Asn	Ser	Phe	Val	Asn	Glu	Ile	Ile	Ser
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Arg Ile Lys Val Thr Thr  
930

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<211> 3145  
<212> DNA  
<213> Homo sapiens

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Mor0003.ST25.txt

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tgtagctca gctagatgct gttgtcagct ttgctcacgt gtcaaattga gcacctgttc 1920
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ataaataaaa tcatgtagtt tgtgg 3145

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<210> 13
<211> 756
<212> PRT
<213> Homo sapiens

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<400> 13

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Met Ser Phe Val Ala Gly Val Ile Arg Arg Leu Asp Glu Thr Val Val
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Asn Arg Ile Ala Ala Gly Glu Val Ile Gln Arg Pro Ala Asn Ala Ile
20          25          30

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Lys Glu Met Ile Glu Asn Cys Leu Asp Ala Lys Ser Thr Ser Ile Gln
35          40          45

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Val Ile Val Lys Glu Gly Gly Leu Lys Leu Ile Gln Ile Gln Asp Asn
50          55          60

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Mor0003.ST25.txt

Gly Thr Gly Ile Arg Lys Glu Asp Leu Asp Ile Val Cys Glu Arg Phe  
 65 70 75 80  
 Thr Thr Ser Lys Leu Gln Ser Phe Glu Asp Leu Ala Ser Ile Ser Thr  
 85 90 95  
 Tyr Gly Phe Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala His  
 100 105 110  
 Val Thr Ile Thr Thr Lys Thr Ala Asp Gly Lys Cys Ala Tyr Arg Ala  
 115 120 125  
 Ser Tyr Ser Asp Gly Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly  
 130 135 140  
 Asn Gln Gly Thr Gln Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala  
 145 150 155 160  
 Thr Arg Arg Lys Ala Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile  
 165 170 175  
 Leu Glu Val Val Gly Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe  
 180 185 190  
 Ser Val Lys Lys Gln Gly Glu Thr Val Ala Asp Val Arg Thr Leu Pro  
 195 200 205  
 Asn Ala Ser Thr Val Asp Asn Ile Arg Ser Ile Phe Gly Asn Ala Val  
 210 215 220  
 Ser Arg Glu Leu Ile Glu Ile Gly Cys Glu Asp Lys Thr Leu Ala Phe  
 225 230 235 240  
 Lys Met Asn Gly Tyr Ile Ser Asn Ala Asn Tyr Ser Val Lys Lys Cys  
 245 250 255  
 Ile Phe Leu Leu Phe Ile Asn His Arg Leu Val Glu Ser Thr Ser Leu  
 260 265 270  
 Arg Lys Ala Ile Glu Thr Val Tyr Ala Ala Tyr Leu Pro Lys Asn Thr  
 275 280 285  
 His Pro Phe Leu Tyr Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp  
 290 295 300  
 Val Asp Val His Pro Thr Lys His Glu Val His Phe Leu His Glu Glu  
 305 310 315 320  
 Ser Ile Leu Glu Arg Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly  
 325 330 335

Mor0003.ST25.txt

Ser Asn Ser Ser Arg Met Tyr Phe Thr Gln Thr Leu Leu Pro Gly Leu  
340 345 350

Ala Gly Pro Ser Gly Glu Met Val Lys Ser Thr Thr Ser Leu Thr Ser  
355 360 365

Ser Ser Thr Ser Gly Ser Ser Asp Lys Val Tyr Ala His Gln Met Val  
370 375 380

Arg Thr Asp Ser Arg Glu Gln Leu Lys Asp Ala Phe Leu Gln Pro Leu  
385 390 395 400

Ser Lys Pro Leu Ser Ser Gln Pro Gln Ala Ile Val Thr Glu Asp Lys  
405 410 415

Thr Asp Ile Ser Ser Gly Arg Ala Arg Gln Gln Asp Glu Glu Met Leu  
420 425 430

Glu Leu Pro Ala Pro Ala Glu Val Ala Ala Lys Asn Gln Ser Leu Glu  
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Gly Asp Thr Thr Lys Gly Thr Ser Glu Met Ser Glu Lys Arg Gly Pro  
450 455 460

Thr Ser Ser Asn Pro Arg Lys Arg His Arg Glu Asp Ser Asp Val Glu  
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Met Val Glu Asp Asp Ser Arg Lys Glu Met Thr Ala Ala Cys Thr Pro  
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Arg Arg Arg Ile Ile Asn Leu Thr Ser Val Leu Ser Leu Gln Glu Glu  
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Ile Asn Glu Gln Gly His Glu Val Leu Arg Glu Met Leu His Asn His  
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Ser Phe Val Gly Cys Val Asn Pro Gln Trp Ala Leu Ala Gln His Gln  
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Thr Lys Leu Tyr Leu Leu Asn Thr Thr Lys Leu Ser Glu Glu Leu Phe  
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Tyr Gln Ile Leu Ile Tyr Asp Phe Ala Asn Phe Gly Val Leu Arg Leu  
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Ser Glu Pro Ala Pro Leu Phe Asp Leu Ala Met Leu Ala Leu Asp Ser  
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Pro Glu Ser Gly Trp Thr Glu Glu Asp Gly Pro Lys Glu Gly Leu Ala  
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Glu Tyr Ile Val Glu Phe Leu Lys Lys Lys Ala Glu Met Leu Ala Asp  
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Tyr Phe Ser Leu Glu Ile Asp Glu Glu Gly Asn Leu Ile Gly Leu Pro  
625 630 635 640

Leu Leu Ile Asp Asn Tyr Val Pro Pro Leu Glu Gly Leu Pro Ile Phe  
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Ile Leu Arg Leu Ala Thr Glu Val Asn Trp Asp Glu Glu Lys Glu Cys  
660 665 670

Phe Glu Ser Leu Ser Lys Glu Cys Ala Met Phe Tyr Ser Ile Arg Lys  
675 680 685

Gln Tyr Ile Ser Glu Glu Ser Thr Leu Ser Gly Gln Gln Ser Glu Val  
690 695 700

Pro Gly Ser Ile Pro Asn Ser Trp Lys Trp Thr Val Glu His Ile Val  
705 710 715 720

Tyr Lys Ala Leu Arg Ser His Ile Leu Pro Pro Lys His Phe Thr Glu  
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Asp Gly Asn Ile Leu Gln Leu Ala Asn Leu Pro Asp Leu Tyr Lys Val  
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Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp  
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Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp  
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Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
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Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
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Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser  
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<210> 23
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